International Journal of Bioscience and Biochemistry
www.biosciencejournal.net
Online ISSN: 2664-6544; Print ISSN: 2664-6536
Received: 03-07-2019; Accepted: 04-08-2019; Published: 11-08-2019
Volume 1; Issue 2; 2019; Page No. 09-13

Plant hormones as cell signaling component, its mechanism and regulated gene expression

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Abstract
The review study was carried out from different research data to find out the innovative latest information on cell signaling component, mechanism and regulated gene expression in plant and animal growth and development. From the review study results, Auxin, GA, cytokinin, ehylene, ABA hormones in defined concentration of treatment and the gene expression as well as enzyme activities altered. Auxin, GA and ABA regulated proteins were described well and found related new genes. DELLA proteins, ACS4, ACS5, and ACS9, ACS7, type E3 ligase, XBAT32 EIN2 and EIN3, F-box proteins, EIN3-BINDING F-BOX1 (EBF1) and EBF2 protein, E3 ligases, DWA1 and DWA2, CUL4-based CRLs, ABI five binding protein (AFP), MATH-BTB proteins, TIR1/AFB proteins and Aux/IAA proteins were noted from different review data.

Keywords: auxin, GA, ABA, protein, gene, cell signaling, growth

1. Introduction
Cell signaling is the communication process that leads basic activities of cells and coordinates all cell actions in plant, animal and human. The ability of cells to respond to their microenvironment is the basis of development, tissue repair, and immunity, as well as normal tissue homeostasis. By understanding cell signaling, diseases may be treated more effectively and artificial tissues may be created (Smith *et al*, 2015) [1]. In the case of cell signaling in plant, cells communicate to coordinate their activities in response to the changing conditions of light, dark, and temperature that guide the plant's cycle of growth, flowering, and fruiting. Plant cells also communicate to coordinate in their roots, stems, and leaves. In this final section, it can be considered how plant cells signal to one another and how they respond to light. Much less is known about the receptors and intracellular signaling mechanisms involved in cell communication in plants, and it can be concentrated mainly on how these differ from those used by animals or human (Hossain and Uddin, 2018a) [11,12].

1.2 Types of cell signaling
Generally cell signaling process can be classified into mechanical and biochemical process based on the type of the signal. Mechanical signals are the signals having forces exerted on the cell and the forces produced by the cell. Biochemical signals are the signals having biochemical molecules such as proteins, lipids, ions and gases (Miller *et al*. 2013) [2]. It was reported that the types of cell signaling were intracrine signals which were produced by the target cell that stay within the target cell, autocrine signals which were produced by the target cell, were secreted, and affected the target cell itself via receptors, juxtacrine signals target touching cells which signals were transmitted along cell membranes via protein or lipid components integral to the membrane and were capable of affecting either the Emitting cell or cells immediately adjacent, paracrine signals target cells which cells in the vicinity of the emitting cell like Neurotransmitters represent and endocrine signals target distant cells: Endocrine cells produce hormones that travel through the blood to reach all parts of the body. (Hossain, 2018, Hossain and Uddin, 2018b) [11, 12].

1.3 Cell signaling Molecules or Component
Hossain *et al*. (2018) [11-12] stated that hormones are the major signaling molecules of the endocrine system, though they often regulate each other's secretion via local signaling and most are also expressed in tissues for local purposes: Major hormones are auxin, gibberellin, ethylene, cytokinin and abscissic acid.

1.3.1. Auxin (IAA)
Calderón Villalobos *et al*. (2012) [6] state that auxin was directly bound by both TIR1/AFB and an Aux/IAA protein simultaneously and thus created a "coreceptor" complex Additionally, the binding affinity of auxin appeared to be predominantly controlled by the Aux/IAA proteins and not the TIR1/AFB proteins (Calderón Villalobos *et al*., 2012) [6]. A 13-amino acid motif known as the degron located within domain II of Aux/IAA proteins (Ramos *et al*., 2001) contributed to substrate stability and turnover rates that range from approximately 10 to 80 min (Dreher *et al*., 2006). The varied protein-protein interaction affinities between TIR1/AFB proteins and Aux/IAA proteins (Calderón Villalobos *et al*., 2012) [6] combined with distinct spatiotemporal patterns of accumulation (Parry *et al*., 2009; Vernoux *et al*., 2011) [21, 28] might contribute to the broad role of auxin in diverse growth processes. Almost every aspect of plant growth and development was controlled by auxin signaling (Stewart and Nemhauser, 2010). The role of UPS activity in the auxin response had been extensively studied and was well

Established (Santner *et al*., 2009; Shan *et al*., 2012) [24]. Figure 1 Showed the auxin signaling in plant (Vanneste and Friml, 2012) [31].

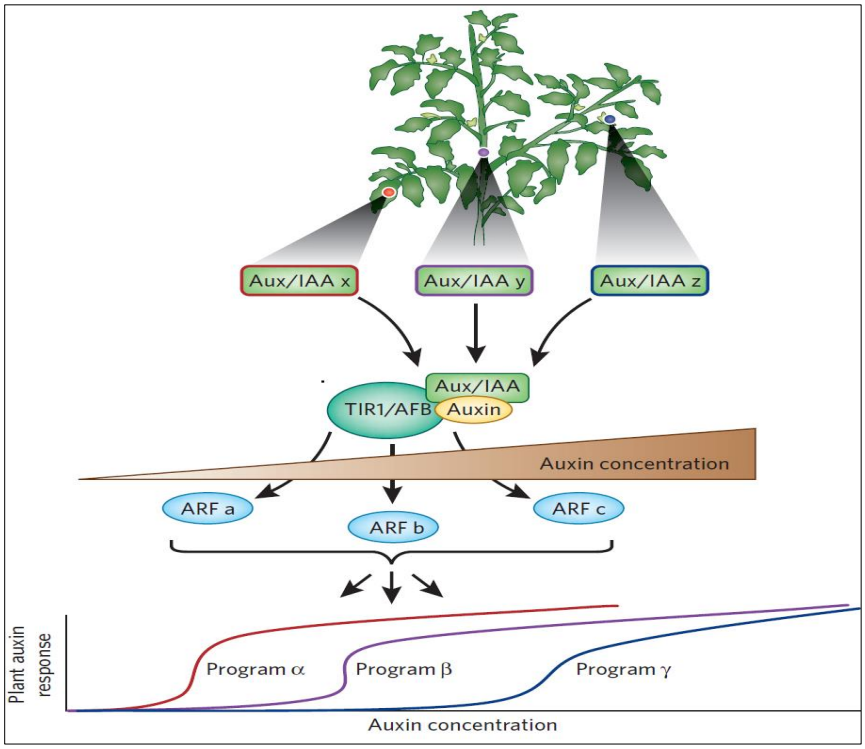

Fig 1: Auxin signaling in plant (www.nature.com/nchembio/journal) https://www.google.co.uk/search?q=auxin+signaling+in+plant&safe=strict&source=lnms&tbm (Vanneste and Friml, 2012).

1.3.2. Gibberellic Acid (GA3)

Gao *et al*. (2011) [13] reported that SCF-mediated regulation had been shown for GA signaling. The effects of GA included promotion of seed germination, stimulation of organ elongation, and induction of flowering. GA was perceived by a protein called gibberellin insensitive dwarf1 (GID1). GA binding to GID1 resulting in binding to nucleus-localized growth repressors called DELLA proteins (Ueguchi-Tanaka *et al*., 2005; Nakajima *et al*., 2006; Willige *et al*., 2007). This tripartite GID-GA-DELLA complex was subsequently targeted for ubiquitylation by SCFSLY1/SNZ E3 ligases, resulting in degradation of the DELLAs (Gao *et al*., 2011) [13]. This scenario was reminiscent of UPS action during auxin and JA-Ile signaling, because DELLA proteins bind and repressed the activity of transcription factors such as the Phytohormone interacting factors (de Lucas *et al*., 2008; Feng *et al*., 2008) [8, 9].

1.3.3. Cytokinin

Hossain *et al* (2018) [11-12] stated that two types of cytokinins: adenine-type cytokinins represented by kinetin, zeatin, and 6-benzylaminopurine, and phenylurea-type cytokinins like diphenylurea and thidiazuron (TDZ). Most adenine-type cytokinins were synthesized in roots (Hossain and Uddin, 2018b) [11, 12]. Cambium and other actively dividing tissues also synthesize cytokinins. The effects of cytokinin include promotion of growth of shoot, stimulation of organ elongation, and induction of flowering. Cytokines are signaling molecules of the immune system, with a primary paracrine or juxtacrine role, though they can during significant immune responses have a strong presence in the circulation, with systemic effect (altering iron metabolism or body temperature). Growth factors can be considered as cytokines or a different class (Hossain and Uddin, 2018b) [11, 12].

1.3.4. Ethylene

Schaller (2012) [26] suggested that ethylene functions as a critical growth regulator and was also important for biotic and abiotic stress responses Many aspects of ethylene signaling are tightly controlled by the UPS (Fig. 1D). First, a number of enzymes involved in ethylene biosynthesis were targeted for proteasomal degradation. This includes (1) type-2 1-aminocyclopropane-1-carboxylic acid synthase proteins (ACS4, ACS5, and ACS9), which were ubiquitylated by ETO1 and ETO-like1/2 BTB ligases (Yoshida *et al*., 2005) [29], and (2) ACS7, a type-3 ACS enzyme that was ubiquitylated by the RING-type E3 ligase XBAT32 (Lyzenga *et al*., 2012) [19]. These degradation mechanisms provided a rapid way to change ethylene concentrations in planta. In the presence of ethylene, ETP expression was repressed, allowing the accumulation of EIN2. Downstream of EIN2 lies EIN3 and EIN3-like1 (EIL1), transcription factors that directly target ethylene-responsive genes. At low ethylene levels, EIN3 and EIL1 were targeted for ubiquitylation and degradation by another pair of F-box proteins, EIN3-BINDING F-BOX1 (EBF1) and EBF2 were also subjected to proteasomal degradation (Guo and Ecker, 2003; Potuschak *et al*., 2003; An *et al*., 2010) [15, 5]. As ethylene levels increased, the stability of EBF1/2 decreased, leading to a buildup of EIN3 and EIL1, thus inducing transcription (An *et al*., 2010) [5].

1.3.5. Abscissic Acid (ABA)

It was reported that the number of E3 ligases involved in ABA signaling was more effectively than for any other hormone to date (Cutler *et al*., 2010; Kim, 2012) [7, 16]. As a result, many aspects of ABA biosynthesis were controlled by protein degradation. ABA played an important roles in many physiological processes, including seed germination and stress responses, both biotic and abiotic. The current understanding of ABA signaling, from receptors to responses, included many intermediate steps and was quite complex (Cutler *et al*., 2010; Kim, 2012) [7, 16]. At least one ligase had been shown to directly impact ABA biosynthesis. In thaliana plant U-BOX44 (AtPUB44) regulated the levels of abscissic aldehyde oxidase3, an enzyme that converted abscisic aldehyde to ABA (Raab *et al*., 2009) [23]. Another gene that had been shown to affect ABA levels was XERICO, which encoded a RING-H2 domain-containing protein that could interact with UPS components in yeast, including the F-box tubby lke protein-9 (Ko *et al*., 2006). The levels of ABA insensitive (ABI5), a basic Leu zipper transcription factor, were regulated by at least two different classes of E3 ligases, DWA1 and DWA2, CUL4-based CRLs (Stone *et al*., 2006; Lee *et al*., 2010). The nucleus-localized ABI five binding protein (AFP) family appears to promote ABI5 degradation in nuclear bodies in concert with the RING protein COP1, although it was not exactly clear how this process occurs (Lopez-Molina *et al*., 2003). A small family of CUL3-based E3 ligases designated CRLBPM had recently been found to play a key role in ABA signaling by directing the proteasomal degradation of the class I homeobox-Leu zipper (HD-ZIP) transcription factor ATHB6 (Lechner *et al*., 2011) [17]. Furthermore, all six MATH-BTB proteins could interacted with three different HD-ZIPI transcription factors (ATHB5, ATHB6, and ATHB16), suggesting that this family of E3 ligases may regulated other processes as well (Lechner *et al*., 2011) [17].

1.4. Signaling mechanism

Dinasarapu *et al* (2011) [3] described the cell signaling mechanism shown in Fig. 2.

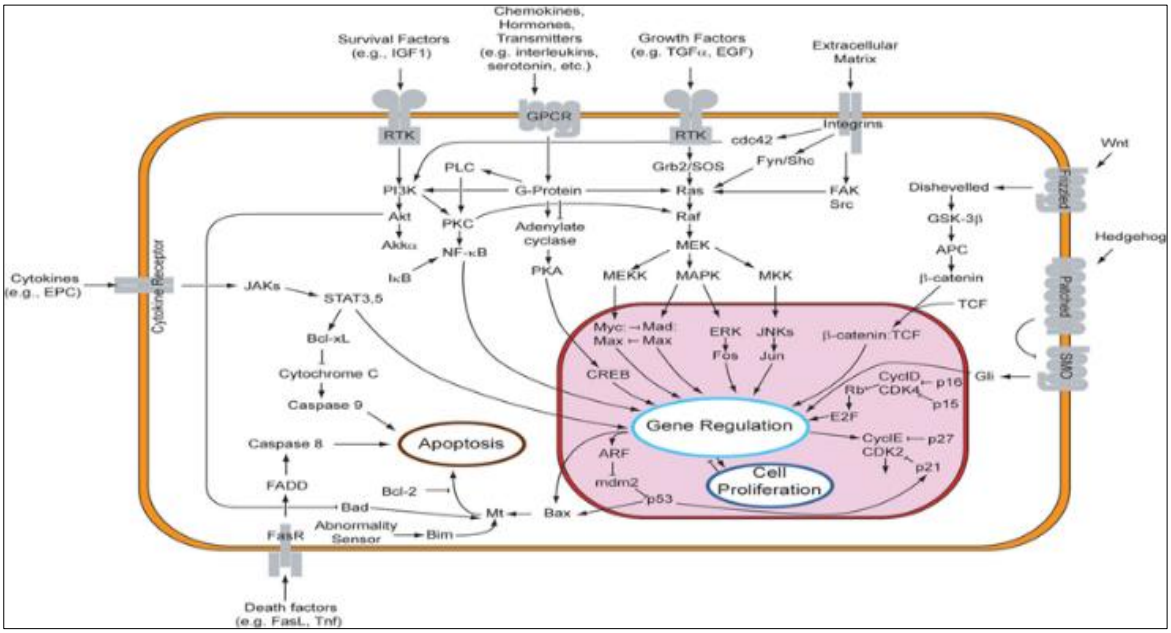

Fig 2: Cell signal transduction pathways (https://en.wikipedia.org/wiki/Cell_signaling#/media/File:Signal_transduction_pathways.png), (Dinasarapu *et al*. 2011) [3]

A signal transduction mechanism or pathway has been shown in Figure 1. This pathway involves the change of protein to protein interactions inside the cell, induced by an external signal. Many growth factors bind to receptors at the cell surface and stimulate cells to progress through the cell cycle and division. Several of these receptors are kinases that start to phosphorylate themselves and other proteins when binding to a ligand. This phosphorylation can generate a binding site for a different protein and thus induce protein to protein interaction. In Figure 1, the ligand (called epidermal growth factor (EGF)) binds to the receptor (called EGFR). This activates the receptor to phosphorylate itself. The phosphorylated receptor binds to an adaptor protein (GRB2), which couples the signal to further downstream signaling processes. For example, one of the signal transduction pathways that are activated is called the mitogen-activated protein kinase (MAPK) pathway. The signal transduction component labeled as MAPK in the pathway was originally called ERK, so the pathway is called the MAPK/ERK pathway. The MAPK protein is an enzyme, a protein kinase that can attach phosphate to target proteins such as the transcription factor MYC and, thus, alter gene transcription and, ultimately, cell cycle progression. Many cellular proteins are activated downstream of the growth factor receptors for example, EGFR that initiate this signal transduction pathway.

1.7. Hormonal regulation of Gene Expression

In mammals hormones can be proteins or steroids. The protein hormones do not enter the cell, but bind to receptors in the cell membrane and mediate gene expression through intermediate molecules. Steroids, though actually enter the cell and interact with steroid receptor proteins to control gene expression. Glucocorticoid hormone is one type of steroid whose method of

controlling gene expression has been determined. The steroid interacts with a receptor protein, and this interaction serves two function. First, binding stimulates the release of the protein Hsp90 that is bound to the receptor protein. When Hsp90 is bound to the receptor protein, gene expression is not activated. This would be expected, if the steroid is the signal required for the expression of specific genes in the tissue. A number of steroid receptor proteins have been characterized, and a number of features are in common among them. First, the N-teriminal region of the protein is required to activate transcription in some manner, but the mechanism is not known. This is the least conserved region among the eight proteins. The central portion of the protein is required for DNA binding, and this region is highly conserved (42-94% amino acid). The C-terminal region is required for steroid binding and is moderately conserved (15-52% amino acid). This overall conservation suggests that an ancestral gene may have been the model for each of these genes (NDSU, 1997).

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